



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 148568

TO: Nita M Minnifield
Location: 3c01 / 3c18
Monday, March 28, 2005
Art Unit: 1645
Phone: 571-272-0860
Serial Number: 09 / 970076

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-22504

jan.delaval@uspto.gov

Search Notes

148868

From: Chan, Christina
Sent: Tuesday, March 22, 2005 4:42 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: interference

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, March 22, 2005 4:38 PM
To: Chan, Christina
Subject: interference

Christina, please approve, 2 month amdt.

STIC

09/970076

Please do an interference sequence search on SEQ ID NO: 2, 6, 8 and 10 of the above application.

Please search against aa and nt databases.

Please provide a paper copy of the results.

Thanks,
Minnifield

STAFF USE ONLY

Searcher:
Searcher Phone: 2- 2504
Date Searcher Picked up: 3/23/05
Date Completed: 3/28/05
Searcher Prep/Rev. Time: 15
Online Time: 20

Type of Search

NA#: ✓ AA#: ✓
Interference: ✓ SPDI:
S/L: Oligomer:
Encode/Transl:
Structure#: Text:
Inventor: Litigation:

RECEIVED
MAR 22 2005
STIC

Vendors and cost where applicable

STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
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Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: March 25, 2005, 08:40:30 ; Search time 673.964 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-2
Perfect score: 1914
Sequence: 1 MATARRALGIGQWLSLAT.....VIIKEVPPPPAESSEENKIK 368

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US09970076@cgn_1_1215 @runat_23032005_062531_9526
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FPGAPOP=6 -FPGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1914	100.0	1454	17	US-10-133-937-58	Sequence 58, Appl
2	1914	100.0	1454	17	US-10-159-563-58	Sequence 58, Appl
3	1894	99.0	5540	10	US-09-918-715-176	Sequence 176, App
4	1894	99.0	5540	10	US-09-918-715-231	Sequence 231, App
5	1894	99.0	5540	15	US-10-301-822-198	Sequence 198, App
6	1894	99.0	5540	18	US-10-474-794-176	Sequence 176, App
7	1894	99.0	5540	18	US-10-474-794-231	Sequence 231, App
8	1793	93.7	5220	10	US-09-918-715-186	Sequence 186, App
9	1793	93.7	5220	10	US-09-918-715-300	Sequence 300, App
10	1793	93.7	5220	18	US-10-474-794-186	Sequence 186, App
11	1793	93.7	5220	18	US-10-474-794-300	Sequence 300, App
12	1661	86.8	1674	15	US-10-038-307-17	Sequence 17, Appl
13	1661	86.8	1674	15	US-10-201-292-17	Sequence 17, Appl
14	1650	86.2	1650	15	US-10-038-307-13	Sequence 13, Appl
15	1650	86.2	1650	15	US-10-038-307-15	Sequence 15, Appl
16	1650	86.2	1650	15	US-10-201-292-13	Sequence 13, Appl
17	1650	86.2	1650	15	US-10-201-292-15	Sequence 15, Appl
18	1649	86.2	1649	15	US-10-038-307-23	Sequence 23, Appl
19	1649	86.2	1649	15	US-10-201-292-23	Sequence 23, Appl
20	1649	86.2	1649	15	US-10-038-307-19	Sequence 19, Appl
21	1649	86.2	1649	15	US-10-201-292-19	Sequence 19, Appl
22	1649	86.2	2272	10	US-09-796-753-11	Sequence 11, Appl
23	1649	86.2	2272	15	US-10-038-307-1	Sequence 1, Appl
24	1649	86.2	2272	15	US-10-201-292-1	Sequence 1, Appl
25	1649	86.2	2353	14	US-10-198-846-9957	Sequence 9957, Ap
26	1640	85.7	1650	15	US-10-038-307-9	Sequence 9, Appl
27	1640	85.7	1650	15	US-10-201-292-9	Sequence 9, Appl
28	1636	85.5	1008	15	US-10-038-307-25	Sequence 25, Appl
29	1636	85.5	1008	15	US-10-201-292-25	Sequence 25, Appl
30	1634.5	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl
31	1634.5	85.4	1047	15	US-10-201-292-21	Sequence 21, Appl
32	1548	80.9	1698	17	US-10-062-674-1757	Sequence 1757, Ap
33	1520	79.4	2397	17	US-10-062-674-1757	Sequence 1757, Ap
34	1509	78.8	1823	15	US-10-038-307-11	Sequence 11, Appl
35	1509	78.8	1823	15	US-10-201-292-11	Sequence 11, Appl
36	1423	74.3	1534	15	US-10-037-270-8	Sequence 8, Appl
37	1392	72.7	1609	17	US-10-117-722-8	Sequence 8, Appl
38	1392	72.7	1609	17	US-10-357-930-30300	Sequence 30300, A
39	1392	72.7	1718	18	US-10-201-292-31	Sequence 31, Appl
40	1313	68.6	1464	15	US-10-201-292-27	Sequence 27, Appl
41	1193	62.3	1401	15	US-10-201-292-29	Sequence 29, Appl
42	1193	62.3	2234	17	US-10-104-047-669	Sequence 669, App
43	962.5	50.3	2234	17	US-10-368-087-9	Sequence 9, Appl
44	962.5	50.3	4081	16	US-09-796-753-51	Sequence 51, Appl
45	957.5	50.0	3677	10		

ALIGNMENTS

RESULT 1
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613-56US01
; CURRENT APPLICATION NUMBER: US/10/133, 937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 25, 2005, 06:07:28 ; Search time 116.423 Seconds

(without alignments)
3063.887 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131

Sequence: 1 MSFVSTRGTTLMKLTEDR.....STSGFKGNHSHCLPARPHT 218

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_Patents_NA -Qfmt=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database :

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5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131	100.0	1609	4	US-09-620-312D-8
2	506	44.7	1492	4	Sequence 297, Appl
3	389	34.4	3981	4	Sequence 250, Appl
4	128.5	11.4	3519	1	Sequence 45, Appl
5	128.5	11.4	3519	1	Sequence 45, Appl
6	128.5	11.4	3519	1	Sequence 45, Appl
7	128.5	11.4	3519	1	Sequence 45, Appl
8	128.5	11.4	3519	1	Sequence 45, Appl
9	128.5	11.4	3519	2	US-08-482-293A-45
10	128.5	11.4	3519	3	Sequence 45, Appl
11	128.5	11.4	3519	3	US-09-193-043-45
12	128.5	11.4	3519	4	US-09-350-259-45

13	128.5	11.4	3803	1	US-08-485-618-52
14	128.5	11.4	3803	1	US-08-362-652-52
15	128.5	11.4	3803	1	US-08-605-672-52
16	128.5	11.4	3803	2	US-08-482-293A-52
17	128.5	11.4	3803	2	US-08-943-363-52
18	128.5	11.4	3803	3	US-09-193-043-52
19	128.5	11.4	3803	3	US-09-688-307A-52
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21	122	10.8	3528	1	US-08-286-889-36
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23	122	10.8	3528	1	US-08-362-652-36
24	122	10.8	3528	1	US-08-605-672-36
25	122	10.8	3528	2	US-08-482-293A-36
26	122	10.8	3528	2	US-08-943-363-36
27	122	10.8	3528	3	US-09-193-043-36
28	122	10.8	3528	3	US-09-688-307A-36
29	122	10.8	3528	4	US-09-350-259-36
30	122	10.8	3597	1	US-08-485-618-54
31	122	10.8	3597	1	US-08-362-652-54
32	122	10.8	3597	1	US-08-605-672-54
33	122	10.8	3597	2	US-08-482-293A-54
34	122	10.8	3597	2	US-08-943-363-54
35	122	10.8	3597	3	US-09-193-043-54
36	122	10.8	3597	3	US-09-688-307A-54
37	122	10.8	3597	4	US-09-350-259-54
38	114	10.1	2499	1	US-08-485-618-96
39	114	10.1	2499	1	US-08-605-672-96
40	114	10.1	2499	2	US-08-482-293A-96
41	114	10.1	2499	2	US-08-943-363-96
42	114	10.1	2499	3	US-09-193-043-96
43	114	10.1	2499	3	US-09-688-307A-96
44	114	10.1	2499	4	US-09-350-259-96
45	114	10.1	3726	1	US-08-173-497-1

ALIGNMENTS

RESULT 1

US-09-620-312D-8

; Sequence 8, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yunging

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pt_FL_genes Version 1.0

; SEQ ID NO 8

; LENGTH: 1609

; TYPE: DNA

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: March 25, 2005, 08:40:30 ; Search time 399.25 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131

Sequence: 1 MSFVSTRTTLKLTEDR.....STGFKGNSHPCLPAPHT 218

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5522208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09970076/runat_23032005_062531_9526/app_query.fasta_1.2140
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Database : Published Applications NA:

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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1131	100.0	1609	15	US-10-037-270-8
2	1131	100.0	1609	17	US-10-117-722-8
3	1131	100.0	1718	18	US-10-357-930-30300
4	977	86.4	1534	15	US-10-201-292-33
5	966.5	85.5	1608	15	US-10-201-292-35
6	966	85.4	1008	15	US-10-038-307-25
7	966	85.4	1008	15	US-10-201-292-25
8	966	85.4	1047	15	US-10-038-307-21
9	966	85.4	1056	15	US-10-201-292-21
10	966	85.4	1056	15	US-10-038-307-23
11	966	85.4	1056	15	US-10-201-292-23
12	966	85.4	1454	17	US-10-133-937-58
13	966	85.4	1454	17	US-10-159-563-58
14	966	85.4	1623	15	US-10-038-307-11
15	966	85.4	1623	15	US-10-201-292-11
16	966	85.4	1650	15	US-10-038-307-9
17	966	85.4	1650	15	US-10-038-307-13
18	966	85.4	1650	15	US-10-038-307-15
19	966	85.4	1650	15	US-10-201-292-9
20	966	85.4	1650	15	US-10-201-292-13
21	966	85.4	1674	15	US-10-201-292-15
22	966	85.4	1674	15	US-10-038-307-17
23	966	85.4	1674	15	US-10-201-292-17
24	966	85.4	1713	15	US-10-038-307-19
25	966	85.4	1713	15	US-10-201-292-19
26	966	85.4	2272	10	US-09-796-753-11
27	966	85.4	2272	15	US-10-038-307-1
28	966	85.4	2272	15	US-10-201-292-1
29	966	85.4	2353	14	US-10-198-846-9957
30	966	85.4	5540	10	US-09-918-715-176
31	966	85.4	5540	10	US-09-918-715-231
32	966	85.4	5540	18	US-10-301-822-198
33	966	85.4	5540	18	US-10-474-794-176
34	966	85.4	5540	18	US-10-474-794-231
35	960	84.9	5220	10	US-09-918-715-186
36	960	84.9	5220	10	US-09-918-715-300
37	960	84.9	5220	18	US-10-474-794-186
38	960	84.9	5220	18	US-10-474-794-300
39	938	82.9	2397	17	US-10-062-674-1757
40	878	77.6	1464	15	US-10-201-292-31
41	767	67.8	1401	15	US-10-201-292-27
42	767	67.8	1401	15	US-10-201-292-29
43	704	62.2	1650	13	US-10-047-542-98
44	704	62.2	6602	13	US-10-047-542-100
45	571	50.5	454	17	US-10-062-674-417

ALIGNMENTS

RESULT 1
US-10-037-270-8
; Sequence 8, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei

Result No.	Score	Query Match	%	ID				Description
				DB	Length	ID	ID	
1	128.5	11.4	1155	1	US-08-286-889-46	Sequence 46, Appl		
2	128.5	11.4	1155	1	US-08-485-618-46	Sequence 46, Appl		
3	128.5	11.4	1155	1	US-08-362-652-46	Sequence 46, Appl		
4	128.5	11.4	1155	2	US-08-605-672-46	Sequence 46, Appl		
5	128.5	11.4	1155	2	US-08-482-293A-46	Sequence 46, Appl		
6	128.5	11.4	1155	2	US-08-943-363-46	Sequence 46, Appl		
7	128.5	11.4	1155	3	US-09-193-043-46	Sequence 46, Appl		
8	128.5	11.4	1155	4	US-09-350-259-46	Sequence 46, Appl		
9	128.5	11.4	1155	1	US-08-485-618-53	Sequence 46, Appl		
10	128.5	11.4	1161	1	US-08-362-652-53	Sequence 53, Appl		
11	128.5	11.4	1161	2	US-08-605-672-53	Sequence 53, Appl		
12	128.5	11.4	1161	2	US-08-482-293A-53	Sequence 53, Appl		
13	128.5	11.4	1161	2	US-08-943-363-53	Sequence 53, Appl		
14	128.5	11.4	1161	3	US-09-193-043-53	Sequence 53, Appl		
15	128.5	11.4	1161	3	US-09-350-259-53	Sequence 53, Appl		
16	128.5	11.4	1161	4	US-09-688-307A-53	Sequence 53, Appl		
17	128.5	11.4	1161	4	US-09-350-259-53	Sequence 53, Appl		
18	122	10.8	1151	1	US-08-286-889-37	Sequence 37, Appl		
19	122	10.8	1151	1	US-08-485-618-37	Sequence 37, Appl		
20	122	10.8	1151	1	US-08-362-652-37	Sequence 37, Appl		
21	122	10.8	1151	2	US-08-605-672-37	Sequence 37, Appl		
22	122	10.8	1151	2	US-08-482-293A-37	Sequence 37, Appl		
23	122	10.8	1151	2	US-08-943-363-37	Sequence 37, Appl		
24	122	10.8	1151	3	US-09-193-043-37	Sequence 37, Appl		
25	122	10.8	1151	4	US-09-350-259-37	Sequence 37, Appl		
26	122	10.8	1151	4	US-09-688-307A-37	Sequence 37, Appl		
27	122	10.8	1161	1	US-08-485-618-55	Sequence 55, Appl		

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OM protein - protein search, using 'sw model'

Run on: March 23, 2005, 11:43:59 ; Search time 39.9838 Seconds
(without alignment)
1805.230 Million cell updates/sec

Title: US-09-970-076-10
Perfect score: 1131
Sequence: 1 MSFVSTRTGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	977.5	86.4	504	14 US-10-201-292-34	Sequence 34, Appl
2	966	85.4	328	14 US-10-038-307-26	Sequence 26, Appl
3	966	85.4	328	14 US-10-038-307-26	Sequence 26, Appl
4	966	85.4	333	10 US-09-796-753-12	Sequence 12, Appl
5	966	85.4	333	14 US-10-038-307-2	Sequence 2, Appl
6	966	85.4	333	14 US-10-201-292-2	Sequence 2, Appl
7	966	85.4	342	14 US-10-038-307-22	Sequence 22, Appl
8	966	85.4	342	14 US-10-201-292-22	Sequence 22, Appl
9	966	85.4	345	14 US-10-038-307-24	Sequence 24, Appl
10	966	85.4	345	14 US-10-201-292-24	Sequence 24, Appl
11	966	85.4	403	11 US-09-833-245-621	Sequence 621, Appl
12	966	85.4	529	14 US-10-201-292-36	Sequence 36, Appl
13	966	85.4	551	14 US-10-038-307-18	Sequence 18, Appl

14	966	85.4	551	14	US-10-201-292-18	Sequence 18, Appl
15	966	85.4	564	10	US-09-918-715-187	Sequence 187, Appl
16	966	85.4	564	10	US-09-918-715-232	Sequence 232, Appl
17	966	85.4	564	14	US-10-038-307-20	Sequence 20, Appl
18	966	85.4	564	14	US-10-201-292-20	Sequence 20, Appl
19	966	85.4	564	14	US-10-301-822-199	Sequence 199, Appl
20	966	85.4	564	16	US-10-408-765A-1823	Sequence 1823, Appl
21	961	85.0	403	11	US-09-833-245-620	Sequence 620, Appl
22	960	84.9	562	10	US-09-918-715-194	Sequence 194, Appl
23	960	84.9	562	10	US-09-918-715-301	Sequence 301, Appl
24	945	83.6	534	14	US-10-038-307-12	Sequence 12, Appl
25	945	83.6	534	14	US-10-201-292-12	Sequence 12, Appl
26	945	83.6	543	14	US-10-038-307-10	Sequence 10, Appl
27	945	83.6	543	14	US-10-038-307-14	Sequence 14, Appl
28	945	83.6	543	14	US-10-038-307-16	Sequence 16, Appl
29	945	83.6	543	14	US-10-201-292-10	Sequence 10, Appl
30	945	83.6	543	14	US-10-201-292-14	Sequence 14, Appl
31	945	83.6	543	14	US-10-201-292-16	Sequence 16, Appl
32	877	77.5	479	14	US-10-201-292-32	Sequence 32, Appl
33	767	67.8	460	14	US-10-201-292-28	Sequence 28, Appl
34	757	66.9	460	14	US-10-201-292-30	Sequence 30, Appl
35	704	62.2	538	13	US-10-047-542-99	Sequence 99, Appl
36	506	44.7	245	15	US-10-094-749-2134	Sequence 2134, Appl
37	506	44.7	272	15	US-10-264-237-1574	Sequence 1574, Appl
38	506	44.7	488	10	US-09-796-753-52	Sequence 52, Appl
39	506	44.7	488	14	US-10-038-307-6	Sequence 6, Appl
40	506	44.7	488	14	US-10-201-292-6	Sequence 6, Appl
41	506	44.7	488	14	US-10-368-087-16	Sequence 16, Appl
42	506	44.7	488	15	US-10-104-047-2639	Sequence 2639, Appl
43	505	44.7	587	9	US-09-764-870-312	Sequence 312, Appl
44	505	44.7	587	11	US-09-764-875-968	Sequence 968, Appl
45	505	44.7	587	14	US-10-125-540-312	Sequence 312, Appl

ALIGNMENTS

RESULT 1
US-10-201-292-34
; Sequence 34, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-34

Query Match 86.4%; Score 977.5; DB 14; Length 504;
Best Local Similarity 91.1%; Pred. No. 5.4e-96;
Matches 194; Conservative 3; Mismatches 9; Indels 7; Gaps 1;
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DB 80 MSFVSTRTGTTLMKLTEDRQIGLEBQKVLPGDVTYMHGFPFRASEQIYYENRQY 139
QY 61 RTASVIALTDGELHDLFFYSERANRSDLGAIYVCVGVKDFNETQIARADSKDHF 120
DB 140 RTASVIALTDGELHDLFFYSERANRSDLGAIYVCVGVKDFNETQIARADSKDHF 199
QY 121 PVNDGFOALQGIHSHLSIKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVRLCSF 180
DB 200 PVNDGFOALQGIHSHLSIKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVRLCSF 259

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 25, 2005, 06:07:28 ; Search time 177.84 Seconds
(without alignments)
3063.887 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728

Sequence: 1 MATAERRALGIGFQWLSLAT.....TTHCSLHLKIASGPTTAACME 333

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-DB=Issued Patents NA -QMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	80.6	1609	4	US-09-620-312D-8
2	702	40.6	1492	4	US-09-774-528-297
3	646	37.4	3981	1	US-09-799-451-250
4	166	9.6	3519	1	US-08-286-889-45
5	166	9.6	3519	1	US-08-485-618-45
6	166	9.6	3519	1	US-08-362-652-45
7	166	9.6	3519	1	US-08-605-672-45
8	166	9.6	3519	1	US-08-482-293A-45
9	166	9.6	3519	2	US-08-943-363-45
10	166	9.6	3519	3	US-09-193-043-45
11	166	9.6	3519	3	US-09-688-307A-45
12	166	9.6	3519	4	US-09-350-259-45

13	166	9.6	3803	1	US-08-485-618-52	Sequence 52, Appl
14	166	9.6	3803	1	US-08-362-652-52	Sequence 52, Appl
15	166	9.6	3803	1	US-08-605-672-52	Sequence 52, Appl
16	166	9.6	3803	2	US-08-482-293A-52	Sequence 52, Appl
17	166	9.6	3803	2	US-08-943-363-52	Sequence 52, Appl
18	166	9.6	3803	3	US-09-193-043-52	Sequence 52, Appl
19	166	9.6	3803	3	US-09-688-307A-52	Sequence 52, Appl
20	166	9.6	3803	4	US-09-350-259-52	Sequence 52, Appl
21	159.5	9.2	2499	1	US-08-485-618-96	Sequence 96, Appl
22	159.5	9.2	2499	1	US-08-605-672-96	Sequence 96, Appl
23	159.5	9.2	2499	2	US-08-482-293A-96	Sequence 96, Appl
24	159.5	9.2	2499	2	US-08-943-363-96	Sequence 96, Appl
25	159.5	9.2	2499	3	US-09-193-043-96	Sequence 96, Appl
26	159.5	9.2	2499	3	US-09-688-307A-96	Sequence 96, Appl
27	159.5	9.2	2499	4	US-09-350-259-96	Sequence 96, Appl
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29	159.5	9.2	3528	1	US-08-485-618-36	Sequence 36, Appl
30	159.5	9.2	3528	1	US-08-362-652-36	Sequence 36, Appl
31	159.5	9.2	3528	1	US-08-605-672-36	Sequence 36, Appl
32	159.5	9.2	3528	2	US-08-482-293A-36	Sequence 36, Appl
33	159.5	9.2	3528	2	US-08-943-363-36	Sequence 36, Appl
34	159.5	9.2	3528	3	US-09-193-043-36	Sequence 36, Appl
35	159.5	9.2	3528	3	US-09-688-307A-36	Sequence 36, Appl
36	159.5	9.2	3528	4	US-09-350-259-36	Sequence 36, Appl
37	159.5	9.2	3597	1	US-08-485-618-54	Sequence 54, Appl
38	159.5	9.2	3597	1	US-08-362-652-54	Sequence 54, Appl
39	159.5	9.2	3597	1	US-08-605-672-54	Sequence 54, Appl
40	159.5	9.2	3597	2	US-08-482-293A-54	Sequence 54, Appl
41	159.5	9.2	3597	2	US-08-943-363-54	Sequence 54, Appl
42	159.5	9.2	3597	3	US-09-193-043-54	Sequence 54, Appl
43	159.5	9.2	3597	3	US-09-688-307A-54	Sequence 54, Appl
44	159.5	9.2	3597	4	US-09-350-259-54	Sequence 54, Appl
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ALIGNMENTS

RESULT 1

US-09-620-312D-8

; Sequence 8, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yungqing

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pt_FL_genes Version 1.0

; SEQ ID NO 8

; LENGTH: 1609

; TYPE: DNA

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: March 25, 2005, 08:40:30 ; Search time 609.864 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-8
Perfect score: 1728
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5552208 seqs, 297965951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	100.0	1713	15	US-10-038-307-19
2	1728	100.0	1713	15	US-10-201-292-19
3	1728	100.0	2272	10	US-09-796-753-11
4	1728	100.0	2272	15	US-10-038-307-1
5	1728	100.0	2272	15	US-10-201-292-1
6	1728	100.0	2353	14	US-10-198-846-9957
7	1718	99.4	1056	15	US-10-038-307-23
8	1718	99.4	1056	15	US-10-201-292-23
9	1713.5	99.2	1047	15	US-10-038-307-21
10	1713.5	99.2	1047	15	US-10-201-292-21
11	1650.5	95.5	1674	15	US-10-038-307-17
12	1650.5	95.5	1674	15	US-10-201-292-17
13	1649	95.4	1454	17	US-10-133-937-58
14	1649	95.4	1454	17	US-10-159-563-58
15	1649	95.4	1650	15	US-10-038-307-13
16	1649	95.4	1650	15	US-10-038-307-15
17	1649	95.4	1650	15	US-10-201-292-13
18	1649	95.4	1650	15	US-10-201-292-15
19	1649	95.4	5540	10	US-09-918-715-176
20	1649	95.4	5540	10	US-09-918-715-231
21	1649	95.4	5540	15	US-10-301-822-198
22	1649	95.4	5540	18	US-10-474-794-176
23	1649	95.4	5540	18	US-10-474-794-231
24	1639	94.8	1650	15	US-10-038-307-9
25	1639	94.8	1650	15	US-10-201-292-9
26	1636	94.7	1008	15	US-10-038-307-25
27	1636	94.7	1008	15	US-10-201-292-25
28	1599	92.5	2397	17	US-10-062-674-1757
29	1556	90.0	1608	15	US-10-201-292-35
30	1553	89.9	5220	10	US-09-918-715-186
31	1553	89.9	5220	10	US-09-918-715-300
32	1553	89.9	5220	18	US-10-474-794-186
33	1553	89.9	5220	18	US-10-474-794-300
34	1508	87.3	1623	15	US-10-038-307-11
35	1508	87.3	1623	15	US-10-201-292-11
36	1423	82.3	1534	15	US-10-201-292-33
37	1392	80.6	1609	15	US-10-037-270-8
38	1392	80.6	1609	17	US-10-117-722-8
39	1392	80.6	1718	18	US-10-357-930-30300
40	1313	76.0	1464	15	US-10-201-292-31
41	1193	69.0	1401	15	US-10-201-292-27
42	1193	69.0	1401	15	US-10-201-292-29
43	903	52.3	1650	13	US-10-047-542-98
44	903	52.3	6602	13	US-10-047-542-100
45	800.5	46.3	2234	17	US-10-104-047-669

ALIGNMENTS

RESULT 1
US-10-038-307-19
; Sequence 19, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-19

Result No.	Query			DB	ID	Description
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1	166	9.6	1155	1	US-08-286-889-46	Sequence 46, Appl
2	166	9.6	1155	1	US-08-485-618-46	Sequence 46, Appl
3	166	9.6	1155	1	US-08-362-652-46	Sequence 46, Appl
4	166	9.6	1155	2	US-08-605-672-46	Sequence 46, Appl
5	166	9.6	1155	2	US-08-482-293A-46	Sequence 46, Appl
6	166	9.6	1155	2	US-08-943-363-46	Sequence 46, Appl
7	166	9.6	1155	3	US-09-193-043-46	Sequence 46, Appl
8	166	9.6	1155	4	US-09-688-307A-46	Sequence 46, Appl
9	166	9.6	1155	4	US-09-350-259-46	Sequence 46, Appl
10	166	9.6	1161	1	US-08-485-618-53	Sequence 53, Appl
11	166	9.6	1161	1	US-08-362-652-53	Sequence 53, Appl
12	166	9.6	1161	2	US-08-605-672-53	Sequence 53, Appl
13	166	9.6	1161	2	US-08-482-293A-53	Sequence 53, Appl
14	166	9.6	1161	2	US-08-943-363-53	Sequence 53, Appl
15	166	9.6	1161	3	US-09-193-043-53	Sequence 53, Appl
16	166	9.6	1161	4	US-09-688-307A-53	Sequence 53, Appl
17	166	9.6	1161	4	US-09-350-259-53	Sequence 53, Appl
18	159.5	9.2	1151	1	US-08-286-889-37	Sequence 37, Appl
19	159.5	9.2	1151	1	US-08-485-618-37	Sequence 37, Appl
20	159.5	9.2	1151	1	US-08-362-652-37	Sequence 37, Appl
21	159.5	9.2	1151	2	US-08-605-672-37	Sequence 37, Appl
22	159.5	9.2	1151	2	US-08-482-293A-37	Sequence 37, Appl
23	159.5	9.2	1151	2	US-08-943-363-37	Sequence 37, Appl
24	159.5	9.2	1151	3	US-09-193-043-37	Sequence 37, Appl
25	159.5	9.2	1151	4	US-09-688-307A-37	Sequence 37, Appl
26	159.5	9.2	1151	4	US-09-350-259-37	Sequence 37, Appl
27	159.5	9.2	1161	1	US-08-173-497-2	Sequence 2, Appl

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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:43:59 ; Search time 61.0762 Seconds

(without alignments)
1805.230 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728

Sequence: 1 MATAERRALLGIGFQWLSLAT.....TTHCSLHKIASGPTTAACME 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	1728	100.0	333	14	US-10-201-292-2
4	1728	100.0	564	14	US-10-038-307-20
5	1728	100.0	564	14	US-10-201-292-20
6	1718	99.4	345	14	US-10-038-307-24
7	1718	99.4	345	14	US-10-201-292-24
8	1713.5	99.2	342	14	US-10-038-307-22
9	1713.5	99.2	342	14	US-10-201-292-22
10	1650.5	95.5	551	14	US-10-038-307-18
11	1650.5	95.5	551	14	US-10-201-292-18
12	1649	95.4	403	11	US-09-833-245-621
13	1649	95.4	564	10	US-09-918-715-187

Sequence 232, App
Sequence 199, App
Sequence 1823, App
Sequence 620, App
Sequence 26, Appl
Sequence 26, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 194, App
Sequence 301, App
Sequence 12, Appl
Sequence 12, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 28, Appl
Sequence 30, Appl
Sequence 99, Appl
Sequence 52, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 16, Appl
Sequence 2639, App
Sequence 312, App
Sequence 968, App
Sequence 312, App
Sequence 54, Appl
Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 25, 2005, 06:07:28 ; Search time 301.206 Seconds
(without alignments)
3063.887 Million cell updates/sec

Title: US-09-970-076-6
Perfect score: 3025
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database :

Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2022	66.8	3981	4	US-09-799-451-250
2	1392	46.0	1609	4	US-09-620-312D-8
3	1306	43.2	1492	4	US-09-774-528-297
c 4	213	7.0	318	3	US-09-165-264-12
c 5	213	7.0	320	3	US-09-165-264-14
c 6	208.5	6.9	34230	4	US-09-949-016-12052
7	208.5	6.9	128470	4	US-09-949-016-13755
c 8	208	6.9	320	3	US-09-165-264-13
9	207.5	6.9	865	4	US-09-270-767-11042
c 10	207.5	6.9	152132	4	US-09-949-016-13845
c 11	207.5	6.9	152145	4	US-09-949-016-12371
c 12	206	6.8	320	3	US-09-165-264-7

13	205.5	6.8	51259	3	US-08-781-891-209	Sequence 209, App
14	205.5	6.8	51259	4	US-09-618-166-209	Sequence 209, App
c 15	205	6.8	320	3	US-09-165-264-11	Sequence 11, Appl
c 16	205	6.8	936	4	US-09-270-767-4464	Sequence 4464, Ap
c 17	205	6.8	936	4	US-09-270-767-19746	Sequence 19746, A
c 18	205	6.8	114793	4	US-10-148-806-3	Sequence 3, Appli
c 19	203	6.7	319	3	US-09-165-264-8	Sequence 8, Appli
20	202.5	6.7	767677	4	US-09-949-016-12147	Sequence 12147, A
21	202.5	6.7	767677	4	US-09-949-016-17361	Sequence 17361, A
22	200.5	6.6	1497	4	US-09-949-016-1237	Sequence 1237, Ap
23	200.5	6.6	12695	4	US-09-949-016-16775	Sequence 16775, A
24	199.5	6.6	324	4	US-08-547-893-234	Sequence 234, App
25	199	6.6	53577	3	US-08-658-136-1	Sequence 1, Appli
26	197.5	6.5	22431	4	US-09-949-016-14099	Sequence 14099, A
27	196.5	6.5	15252	4	US-09-949-016-13584	Sequence 13584, A
c 28	196.5	6.5	97195	4	US-09-949-016-12212	Sequence 12212, A
c 29	196.5	6.5	97196	4	US-09-949-016-16971	Sequence 16971, A
30	196	6.5	226	4	US-09-513-999C-12498	Sequence 12498, A
31	195	6.4	16442	3	US-08-781-891-208	Sequence 208, App
32	195	6.4	16442	4	US-09-618-166-208	Sequence 208, App
33	194	6.4	53526	3	US-08-658-136-2	Sequence 2, Appli
c 34	193	6.4	11766	4	US-09-949-016-12531	Sequence 12531, A
c 35	193	6.4	11770	4	US-09-949-016-12720	Sequence 12720, A
c 36	193	6.4	11770	4	US-08-949-016-13487	Sequence 13487, A
c 37	193	6.4	11770	4	US-09-949-016-13488	Sequence 13488, A
c 38	192	6.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
39	191.5	6.3	2230	1	US-08-217-327-5	Sequence 5, Appli
c 40	191.5	6.3	16782	4	US-09-949-016-12791	Sequence 12791, A
c 41	191.5	6.3	39154	4	US-09-949-016-12384	Sequence 12384, A
c 42	191.5	6.3	39154	4	US-09-949-016-12801	Sequence 12801, A
c 43	191.5	6.3	39443	4	US-09-949-016-14326	Sequence 14326, A
c 44	191.5	6.3	39443	4	US-09-949-016-14327	Sequence 14327, A
c 45	191.5	6.3	767677	4	US-09-949-016-12147	Sequence 12147, A

ALIGNMENTS

RESULT 1

US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Kyle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyun

; APPLICANT: Zhang, Jie

; APPLICANT: Xue, Aidong J.

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Ma, Yunging

; APPLICANT: Yamazaki, Victoria

; APPLICANT: Chen, Rui-hong

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wang, Dunrui

; APPLICANT: Yang, Yonghong

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Reena

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6783969el Nucleic Acids and

; FILE OF INVENTION: Polypeptides

; FILE REFERENCE: 803

; CURRENT APPLICATION NUMBER: US/09/799,451

; CURRENT FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 948

; SOFTWARE: pt_FL_genes Version 2.0

; SEQ ID NO 250

; LENGTH: 3981

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: March 25, 2005, 08:40:30 ; Search time 1032.92 Seconds
(without alignments)
3253.936 Million cell updates/sec

Title: US-09-970-076-6
Perfect score: 3025
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3025	100.0	5540	10	US-09-918-715-176
2	3025	100.0	5540	10	US-09-918-715-231
3	3025	100.0	5540	15	US-10-301-822-198
4	3025	100.0	5540	18	US-10-474-794-176
5	3025	100.0	5540	18	US-10-474-794-231
6	2901	95.9	5220	10	US-09-918-715-186
7	2901	95.9	5220	10	US-09-918-715-300
8	2901	95.9	5220	18	US-10-474-794-186
9	2901	95.9	5220	18	US-10-474-794-300
10	2022	66.8	3981	17	US-10-302-172-250
11	2017	66.7	4417	10	US-09-796-753-23
12	2017	66.7	4417	15	US-10-038-307-3
13	2017	66.7	4417	15	US-10-201-292-3
14	1894	62.6	1454	17	US-10-133-937-58
15	1894	62.6	1454	17	US-10-159-563-58
16	1661	54.9	1674	15	US-10-038-307-17
17	1661	54.9	1674	15	US-10-201-292-17
18	1652.5	54.6	1650	15	US-10-038-307-15
19	1652.5	54.6	1650	15	US-10-201-292-15
20	1650.5	54.6	1650	15	US-10-038-307-13
21	1650.5	54.6	1650	15	US-10-201-292-13
22	1650	54.5	2272	10	US-09-796-753-11
23	1650	54.5	2272	15	US-10-038-307-1
24	1650	54.5	2272	15	US-10-201-292-1
25	1650	54.5	2353	14	US-10-198-846-9957
26	1649	54.5	1056	15	US-10-038-307-23
27	1649	54.5	1056	15	US-10-201-292-23
28	1649	54.5	1713	15	US-10-038-307-19
29	1649	54.5	1713	15	US-10-201-292-19
30	1640.5	54.2	1650	15	US-10-038-307-9
31	1640.5	54.2	1650	15	US-10-201-292-9
32	1636	54.1	1008	15	US-10-038-307-25
33	1636	54.1	1008	15	US-10-201-292-25
34	1634.5	54.0	1047	15	US-10-038-307-21
35	1634.5	54.0	1047	15	US-10-201-292-21
36	1557.5	51.5	1608	15	US-10-201-292-35
37	1530	50.6	2397	17	US-10-062-674-1757
38	1509.5	49.9	1623	15	US-10-038-307-11
39	1509.5	49.9	1623	15	US-10-201-292-11
40	1423	47.0	1534	15	US-10-201-292-33
41	1416.5	46.8	2234	17	US-10-104-047-669
42	1416.5	46.8	4081	16	US-10-368-087-9
43	1411.5	46.7	3677	10	US-09-796-753-51
44	1411.5	46.7	3677	15	US-10-038-307-5
45	1411.5	46.7	3677	15	US-10-201-292-5

ALIGNMENTS

RESULT 1
US-09-918-715-176
; Sequence 176, Application US/0918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/0918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:30:49 ; Search time 35.3688 Seconds
(without alignments)
1190.372 Million cell updates/sec

Title: US-09-970-076-6
Perfect score: 3025
Sequence: 1 MATARRALGIGFOWLSLAT.....QAPPNNRAPPSPPPRPSV 564

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	6.6	104	US-09-547-693-235	Sequence 235, App
2	199	6.6	288	US-09-270-767-42632	Sequence 42632, A
3	195	6.4	498	US-09-949-016-7108	Sequence 7108, Ap
4	191.5	6.3	306	US-08-217-327-6	Sequence 6, Appli
5	186	6.1	76	US-09-547-693-233	Sequence 233 App
6	186	6.1	214	US-08-217-327-4	Sequence 4, Appli
7	178.5	5.9	802	US-09-823-240A-2	Sequence 2, Appli
8	175	5.8	294	US-09-270-767-36084	Sequence 36084, A
9	175	5.8	294	US-09-270-767-51301	Sequence 51301, A
10	173.5	5.7	142	US-09-252-991A-24873	Sequence 24873, A
11	173.5	5.7	334	5202236-3	Patent No. 5202236
12	173.5	5.7	334	5202236-3	Patent No. 5202236
13	173.5	5.7	971	US-09-248-796A-19531	Sequence 19531, A
14	172	5.7	553	US-09-949-016-7961	Sequence 7961, Ap
15	171.5	5.7	331	5202236-37	Patent No. 5202236
16	171.5	5.7	331	5202236-37	Patent No. 5202236
17	170	5.6	581	US-09-949-016-9978	Sequence 9978, Ap
18	167.5	5.5	1248	US-09-080-897-2	Sequence 2, Appli
19	167.5	5.5	1248	US-09-323-735-2	Sequence 2, Appli
20	167	5.5	1231	US-08-714-741-41	Sequence 41, Appl
21	166	5.5	1155	US-08-286-889-46	Sequence 46, Appl
22	166	5.5	1155	US-08-485-618-46	Sequence 46, Appl
23	166	5.5	1155	US-08-362-652-46	Sequence 46, Appl
24	166	5.5	1155	US-08-605-672-46	Sequence 46, Appl
25	166	5.5	1155	US-08-482-293A-46	Sequence 46, Appl
26	166	5.5	1155	US-08-943-363-46	Sequence 46, Appl
27	166	5.5	1155	US-09-193-043-46	Sequence 46, Appl

28 166 5.5 1155 4 US-09-588-307A-46 Sequence 46, Appl
29 166 5.5 1155 4 US-09-350-259-46 Sequence 46, Appl
30 166 5.5 1161 1 US-08-485-618-53 Sequence 53, Appl
31 166 5.5 1161 1 US-08-362-652-53 Sequence 53, Appl
32 166 5.5 1161 2 US-08-605-672-53 Sequence 53, Appl
33 166 5.5 1161 2 US-08-482-293A-53 Sequence 53, Appl
34 166 5.5 1161 2 US-08-943-363-53 Sequence 53, Appl
35 166 5.5 1161 3 US-09-193-043-53 Sequence 53, Appl
36 166 5.5 1161 4 US-09-688-307A-53 Sequence 53, Appl
37 166 5.5 1161 4 US-09-350-259-53 Sequence 53, Appl
38 165 5.5 105 4 US-09-547-693-230 Sequence 230, App
39 164 5.4 511 4 US-09-107-433-2904 Sequence 2904, Ap
40 163 5.4 635 1 US-07-832-855-2 Sequence 2, Appli
41 162.5 5.4 203 4 US-09-543-681A-8287 Sequence 8287, Ap
42 162 5.4 559 4 US-10-116-370-2 Sequence 2, Appli
43 162 5.4 567 4 US-09-949-016-10952 Sequence 10952, A
44 161.5 5.3 506 4 US-09-949-016-11282 Sequence 11282, A
45 161.5 5.3 1315 3 US-08-899-595-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-547-693-235
; Sequence 235, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-235

Query Match Best Local Similarity 6.6%; Score 199; DB 4; Length 104;
Matches 38; Conservative 7; Mismatches 33; Indels 2; Gaps 1;
QY 485 TRVKNQPAKYPLNNAYHTSSPPAPIVTPPPAPHCPPPPSPPTLP--P 542
Db 4 TRASPP 63
QY 543 PPQAPPPNRRAPPPPPPPRP 562
Db 64 PPSPPPPPPPPPPPPPPPPP 83

RESULT 2

US-09-270-767-42632
; Sequence 42632, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7325-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42632
; LENGTH: 288
; TYPE: PRT

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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:43:59 ; Search time 103.444 Seconds
(without alignments)
1805.230 Million cell updates/sec

Title: US-09-970-076-6

Perfect score: 3025

Sequence: 1 MATARRALGIGFQWLSLAT.....QAPPPNRRAPPPRRPPSV 564

Scoring table: BLOSUM62

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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pcp.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US10C PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3025	100.0	564	10 US-09-918-715-187	Sequence 187, App
2	3025	100.0	564	10 US-09-918-715-232	Sequence 232, App
3	3025	100.0	564	14 US-10-301-822-199	Sequence 199, App
4	3025	100.0	564	15 US-10-408-765A-1823	Sequence 1823, App
5	2801	95.9	562	10 US-09-918-715-194	Sequence 194, App
6	2901	95.9	562	10 US-09-918-715-301	Sequence 301, App
7	2017	66.7	381	10 US-09-796-753-24	Sequence 24, Appl
8	2017	66.7	381	14 US-10-038-307-4	Sequence 4, Appli
9	2017	66.7	381	14 US-10-201-292-4	Sequence 4, Appli
10	1893.5	62.6	403	11 US-09-833-245-621	Sequence 621, App
11	1874	62.0	403	11 US-09-833-245-620	Sequence 620, App
12	1661	54.9	551	14 US-10-038-307-18	Sequence 18, Appl
13	1661	54.9	551	14 US-10-201-292-18	Sequence 18, Appl

14	1649	54.5	333	10	US-09-796-753-12	Sequence 12, Appl
15	1649	54.5	333	14	US-10-038-307-2	Sequence 2, Appli
16	1649	54.5	333	14	US-10-201-292-2	Sequence 2, Appli
17	1649	54.5	345	14	US-10-038-307-24	Sequence 24, Appl
18	1649	54.5	345	14	US-10-201-292-24	Sequence 24, Appl
19	1649	54.5	564	14	US-10-038-307-20	Sequence 20, Appl
20	1649	54.5	564	14	US-10-201-292-20	Sequence 20, Appl
21	1636	54.1	338	14	US-10-038-307-26	Sequence 26, Appl
22	1636	54.1	338	14	US-10-201-292-26	Sequence 26, Appl
23	1634.5	54.0	342	14	US-10-038-307-22	Sequence 22, Appl
24	1634.5	54.0	342	14	US-10-201-292-22	Sequence 22, Appl
25	1629	53.9	543	14	US-10-038-307-16	Sequence 16, Appl
26	1629	53.9	543	14	US-10-038-307-16	Sequence 16, Appl
27	1629	53.9	543	14	US-10-201-292-14	Sequence 14, Appl
28	1629	53.9	543	14	US-10-201-292-14	Sequence 14, Appl
29	1619	53.5	543	14	US-10-038-307-10	Sequence 10, Appl
30	1619	53.5	543	14	US-10-201-292-10	Sequence 10, Appl
31	1552.5	51.3	529	14	US-10-038-307-36	Sequence 36, Appl
32	1488	49.2	534	14	US-10-038-307-12	Sequence 12, Appl
33	1488	49.2	534	14	US-10-201-292-12	Sequence 12, Appl
34	1434.5	47.4	504	14	US-10-201-292-34	Sequence 34, Appl
35	1416.5	46.8	488	14	US-10-368-087-16	Sequence 16, Appl
36	1416.5	46.8	488	15	US-10-104-047-2639	Sequence 2639, Ap
37	1411.5	46.7	488	10	US-09-796-753-52	Sequence 52, Appl
38	1411.5	46.7	488	14	US-10-038-307-6	Sequence 6, Appli
39	1411.5	46.7	488	14	US-10-201-292-6	Sequence 6, Appli
40	1396.5	46.2	487	10	US-09-796-753-54	Sequence 54, Appl
41	1396.5	46.2	487	14	US-10-038-307-8	Sequence 8, Appli
42	1396.5	46.2	487	14	US-10-201-292-8	Sequence 8, Appli
43	1396.5	46.2	487	14	US-10-368-087-15	Sequence 15, Appl
44	1307	43.2	479	14	US-10-201-292-32	Sequence 32, Appl
45	1206.5	39.9	597	9	US-09-764-870-312	Sequence 312, App

ALIGNMENTS

RESULT 1

US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

Query Match 100.0%; Score 3025; DB 10; Length 564;
Best Local Similarity 100.0%; Pred. No. 5.3e-216;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 EIIYFVEQLAHKFIISPOLRMSFVSTRTTLMKLTEDREQRLQLEELQKVLPGGDTYM 120
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 25, 2005, 06:07:28 ; Search time 196.531 Seconds
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3063.887 Million cell updates/sec

Title: US-09-970-076-2
Perfect score: 1914
Sequence: 1 MATARRALGIGFWLSLAT.....VIVKEVPPPPAESEENKIK 368

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Fgapop 6.0 , Fgapext 7.0
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	72.7	1609	4	US-09-620-312D-8
2	891	46.6	3981	4	US-09-799-451-250
3	859	44.9	1492	4	US-09-774-528-297
4	166	8.7	3519	1	US-08-286-889-45
5	166	8.7	3519	1	US-08-485-618-45
6	166	8.7	3519	1	US-08-362-652-45
7	166	8.7	3519	1	US-08-605-672-45
8	166	8.7	3519	2	US-08-482-293A-45
9	166	8.7	3519	2	US-08-943-363-45
10	166	8.7	3519	3	US-09-193-043-45
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13	166	8.7	3803	1	US-08-485-618-52
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15	166	8.7	3803	2	US-08-605-672-52
16	166	8.7	3803	2	US-08-482-293A-52
17	166	8.7	3803	3	US-08-943-363-52
18	166	8.7	3803	3	US-09-193-043-52
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31	159.5	8.3	3528	1	US-08-605-672-36
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ALIGNMENTS

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; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-bong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 8
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6	166	8.7	1155	2	US-08-943-363-46	Sequence 46, Appl
7	166	8.7	1155	3	US-09-193-043-46	Sequence 46, Appl
8	166	8.7	1155	4	US-09-688-307A-46	Sequence 46, Appl
9	166	8.7	1155	4	US-09-350-259-46	Sequence 46, Appl
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22	159.5	8.3	1151	2	US-08-482-293A-37	Sequence 37, Appl
23	159.5	8.3	1151	2	US-08-943-363-37	Sequence 37, Appl
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25	159.5	8.3	1151	4	US-09-688-307A-37	Sequence 37, Appl
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GenCore version 5.1.6
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Title: US-09-970-076-2

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Total number of hits satisfying chosen parameters: 1407402

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1894	99.0	564	16	US-10-408-765A-1823
5	1889	98.7	403	11	US-09-833-245-621
6	1870	97.7	403	11	US-09-833-245-620
7	1793	93.7	562	10	US-09-918-715-194
8	1793	93.7	562	10	US-09-918-715-301
9	1661	86.8	551	14	US-10-038-307-18
10	1661	86.8	551	14	US-10-201-292-18
11	1649	86.2	333	10	US-09-796-753-12
12	1649	86.2	333	14	US-10-038-307-2
13	1649	86.2	333	14	US-10-201-292-2

14	1649	86.2	345	14	US-10-038-307-24	Sequence 24, Appl
15	1649	86.2	345	14	US-10-201-292-24	Sequence 24, Appl
16	1649	86.2	564	14	US-10-038-307-20	Sequence 20, Appl
17	1649	86.2	564	14	US-10-201-292-20	Sequence 20, Appl
18	1636	85.5	328	14	US-10-038-307-26	Sequence 26, Appl
19	1636	85.5	328	14	US-10-201-292-26	Sequence 26, Appl
20	1634.5	85.4	342	14	US-10-038-307-22	Sequence 22, Appl
21	1634.5	85.4	342	14	US-10-201-292-22	Sequence 22, Appl
22	1629	85.1	543	14	US-10-038-307-14	Sequence 14, Appl
23	1629	85.1	543	14	US-10-038-307-16	Sequence 16, Appl
24	1629	85.1	543	14	US-10-201-292-14	Sequence 14, Appl
25	1629	85.1	543	14	US-10-201-292-16	Sequence 16, Appl
26	1619	84.6	543	14	US-10-038-307-10	Sequence 10, Appl
27	1619	84.6	543	14	US-10-201-292-10	Sequence 10, Appl
28	1548	80.9	529	14	US-10-038-307-36	Sequence 36, Appl
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30	1488	77.7	534	14	US-10-201-292-12	Sequence 12, Appl
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32	1307	68.3	479	14	US-10-201-292-32	Sequence 32, Appl
33	1193	62.3	460	14	US-10-038-307-6	Sequence 6, Appl
34	1183	61.8	460	14	US-10-201-292-30	Sequence 30, Appl
35	962.5	50.3	488	14	US-10-368-087-16	Sequence 16, Appl
36	962.5	50.3	488	15	US-10-104-047-2639	Sequence 2639, Ap
37	957.5	50.0	488	10	US-09-796-753-52	Sequence 52, Appl
38	957.5	50.0	488	14	US-10-038-307-6	Sequence 6, Appl
39	957.5	50.0	488	14	US-10-201-292-6	Sequence 6, Appl
40	938.5	49.0	587	9	US-09-764-870-312	Sequence 312, App
41	938.5	49.0	587	11	US-09-764-875-968	Sequence 968, App
42	938.5	49.0	587	14	US-10-125-540-312	Sequence 312, App
43	936.5	48.9	487	10	US-09-796-753-54	Sequence 54, Appl
44	936.5	48.9	487	14	US-10-038-307-8	Sequence 8, Appl
45	936.5	48.9	487	14	US-10-201-292-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

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; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bert Vogelstein
; APPLICANT: Brad St. Croix
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

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Best Local Similarity 100.0%; Pred. No. 6.6e-182; Indels 0; Gaps 0;
Matches 364; Conservative 0; Mismatches 0;

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